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Substitute for form 1449B/PTO

INFORMATION DISCLOSURE STATEMENT BY APPLICANT

(use as many sheets as necessary)

Sheet	1	of	1
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Complete if Known

Application Number	10/178,782
Filing Date	June 25, 2002
First Named Inventor	Toni Ceccardi et al.
Group Art Unit	1636
Examiner Name	TBA
Attorney Docket Number	CL001242

OTHER PRIOR ART – NON PATENT LITERATURE DOCUMENTS

Examiner Initials	Cite No. 1	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published.	T2
		<p>Results of BLAST search of SEQ ID NO:2 against Derwent (FastAlert and GeneSeqP) and NCBI (pataa) protein patent databases on October 9, 2003.</p>	

Examiner
Signature

Date
Considered

*EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

¹ Applicant's unique citation designation number (optional). ² Applicant is to place a check mark here if English language Translation is attached.

Burden Hour Statement: This form is estimated to take 2.0 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, Washington, DC 20231. **DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO:** Assistant Commissioner for Patents, Washington, DC 20231.



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Re Application of: Toni Ceccardi et al.

Art Unit: 1636

Serial No.: 10/178,782

Examiner: TBA

Filed: June 25, 2002

Atty. Docket: CL001242

For: ISOLATED HUMAN SECRETED PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN SECRETED
PROTEINS, AND USES THEREOF

**Statement Regarding Duty to Disclose Information Material To Patentability Under
37 CFR 1.56 (a) and (b)**

Assistant Commissioner for Patents
Washington, D.C. 20231

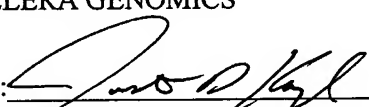
Sir:

Applicants hereby notify the US Patent and Trademark Office of the documents listed on the attached PTO Form SB/08A, which may be deemed relevant to the patentability of the claims of the above application. One copy of each of the listed documents is submitted herewith. The submission of the listed documents is not intended as an admission that any such document constitutes prior art against the claims of the present application.

No fee is due for this submission. However, the Patent and Trademark Office is authorized to charge any necessary fees related to the processing of this application to Deposit Account No. 50-0970.

Respectfully submitted,
CELERA GENOMICS

Date: October 31, 2003

By: 
Justin D. Karjala, Reg No. 43,704

Celera Genomics
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Rockville, MD 20850
Tel: 240-453-3812
Fax: 240-453-3084

Patent Screen Results

Your Fasta Input (protein sequence):

>CL001242, SEQ ID NO:2, October 9, 2003

```
1 MQCLLLTLISM ALVCAIQARD IPQTKQDVEL PKLAGTWYSM AMVASDFSLL
51 ETVEAPLRVN ITSLWPTPEG NLEIILHRCP TSVRFLREHH RCVERTVLAQ
101 KTEDPAVFMV DRRDKKDL CV GHRLDDRSYV FFCMGTTTPR TEPASPTART
151 LEADDKVMEE FISFLRTL PV HMWIFLDVTQ AEEQCRV
```

GENESEQP Blast Report:

BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= CL001242, SEQ ID NO:2, October 9, 2003
(187 letters)

Database: /work/eda3/blast/public/geneseqp_all.fasta
952,616 sequences; 143,563,330 total letters

Sequences producing significant alignments:	Score (bits)	E Value
CRA 222000028409018 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	331	3e-90
CRA 67000131174625 /dataset=GENESEQ /org=Homo sapiens /taxon=96...	173	6e-43
CRA 1000685996856 /dataset=GENESEQ /org=Homo sapiens /taxon=960...	173	6e-43
CRA 1000685996856 /dataset=GENESEQ /org=Homo sapiens /taxon=960...	173	6e-43
CRA 1000685996856 /dataset=GENESEQ /org=Homo sapiens /taxon=960...	173	6e-43
CRA 1000685996856 /dataset=GENESEQ /org=Homo sapiens /taxon=960...	173	6e-43
CRA 335001099106028 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	171	4e-42
CRA 335001099106028 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	171	4e-42
CRA 335001099106028 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	171	4e-42
CRA 335001099185942 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	161	3e-39
CRA 1000686003608 /dataset=GENESEQ /org=Homo sapiens /taxon=960...	147	4e-35
CRA 1000686003608 /dataset=GENESEQ /org=Homo sapiens /taxon=960...	147	4e-35
CRA 335001099310968 /dataset=GENESEQ /org=Synthetic /taxon=0 /m...	137	5e-32
CRA 335001099310966 /dataset=GENESEQ /org=Synthetic /taxon=0 /m...	137	6e-32
CRA 335001099310964 /dataset=GENESEQ /org=Synthetic /taxon=0 /m...	136	1e-31
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CRA 1000685996862 /dataset=GENESEQ /org=Homo sapiens /taxon=960...	134	4e-31
CRA 224000031048966 /dataset=GENESEQ /org=Homo sapiens /taxon=9...	132	2e-30
CRA 66000019966783 /dataset=GENESEQ /org=Bos taurus /taxon=9913...	123	6e-28
CRA 66000019966783 /dataset=GENESEQ /org=Bos sp /taxon=0 /mol_t...	123	6e-28
CRA 1000686172429 /dataset=GENESEQ /org=Bos taurus /taxon=9913 ...	119	2e-26

>CRA|222000028409018 /dataset=GENESEQ /org=Homo sapiens /taxon=9606
/mol_type=aa /date=05-NOV-02 /length=183
/altid=derwent_ac|ABG31900 /altid=derwent_id|ABG31900
/def=Human lipid-associated molecule, LIPAM7
/patent=WO200246418-A2 /pat_section=Claim
Length = 183

Score = 331 bits (839), Expect = 3e-90

Identities = 170/191 (89%), Positives = 171/191 (89%), Gaps = 12/191 (6%)

```
Query: 1  MQCLLLTSLMALVCAIQARDIPQTKQDVELPKLAGTWYSMAMVASDFSLLLETVEAPLRVN 60
          MQCLLLTSLMALVCAIQARDIPQTKQDVELPKLAGTWYSMAMVASDFSLLLETVEAPLRVN
Sbjct: 1  MQCLLLTSLMALVCAIQARDIPQTKQDVELPKLAGTWYSMAMVASDFSLLLETVEAPLRVN 60

Query: 61  ITSLWPTPEGNLEIILHRCPTSVRFLREHHRCVERTVLAQKTEDPAVFMVDR-RDKKDLC 119
          ITSLWPTPEGNLEIILHR                      EHHRCVERTVLAQKTEDPAVFMVDR RDKKDLC
Sbjct: 61  ITSLWPTPEGNLEIILHRW-----EHHRCVERTVLAQKTEDPAVFMVDRSRDKKDLC 112

Query: 120 VGHRLDDRSYVFFCMGTTTPRTE---PASPTARTLEADDKVMEEFISFLRTLPHVMWIFL 176
          VGHRLDDRSYVFFCMGTTTP  +                ARTLEADDKVMEEFISFLRTLPHVMWIFL
Sbjct: 113 VGHRLDDRSYVFFCMGTTTPSADHHTMCQYLARTLEADDKVMEEFISFLRTLPHVMWIFL 172

Query: 177 DVTQAEEQCRV 187
          DVTQAEEQCRV
Sbjct: 173 DVTQAEEQCRV 183
```

Database: /work/eda3/blast/public/geneseqp_all.fasta
Posted date: Mar 2, 2003 3:26 AM
Number of letters in database: 143,563,330
Number of sequences in database: 952,616

Lambda	K	H
0.325	0.136	0.419

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 52529493

Number of Sequences: 952616

Number of extensions: 1921517

Number of successful extensions: 5458

Number of sequences better than 1.0e-08: 21

Number of HSP's better than 0.0 without gapping: 19

Number of HSP's successfully gapped in prelim test: 2

Number of HSP's that attempted gapping in prelim test: 5394

Number of HSP's gapped (non-prelim): 21

length of query: 187

length of database: 143,563,330

effective HSP length: 50

effective length of query: 137

effective length of database: 95,932,530

effective search space: 13142756610

effective search space used: 13142756610

T: 11

A: 40

X1: 15 (7.0 bits)

X2: 38 (14.8 bits)

X3: 64 (24.9 bits)

S1: 40 (21.6 bits)

S2: 144 (60.5 bits)